



ALIGNMENT REPORT OF UNTITLED, USING CLUSTAL METHOD WITH PAM250 RESIDUE WEIGHT TABLE.

	10	20	30	40	
1	MADHSFSDGVPSPSDSVEAAAKNAASNTTEKLLTDQVMQNP	Q99733 IN SwissProt-1.pro			
1	MAENSLSGGPADSVAAAKNAASNTTEKLLTDQVMQNPQ	3319977 IN GenPept-1.pro			
1	MAESENRRKELSESQAAGNQMVEEGLGEHLERGEDAAAG	5931610 IN GenPept-1.pro			
1	MADSENGPAPESPQAAGAAAEAAEVEVMAEQGGDCDSA	hNARC10C orf1-1.pro			
1	MAESVDHKELESSESNQEEELLGSQVMAEGPGESEGV	P51860 IN SwissProt-1.pro			
1	MTNDNI-----AVTDLTSALENREENRAD-----	1161252 IN GenPept-1.pro			
	50	60	70	80	
37	-----VLAALQERLDNVPHTPSS-----	Q99733 IN SwissProt-1.pro			
37	-----VLAALQERLDNVPSTPSS-----	3319977 IN GenPept-1.pro			
41	LGDGKCGEEA-AAAGLGEENGEDTAAGSGEDGKKGGDT	5931610 IN GenPept-1.pro			
41	AGDP-----DSAAAGQMAEEPQTPAENAPK-----	hNARC10C orf1-1.pro			
41	PGDGGQHGEETVAAAGVGEEG-KGEEAAGSGEDAGKCGGT	P51860 IN SwissProt-1.pro			
23	-----LVNALKSKIQSLAGA-----	1161252 IN GenPept-1.pro			
	90	100	110	120	
55	-----YIETLPKAVKKRRINALKQLQ	Q99733 IN SwissProt-1.pro			
55	-----YIETLPKAVKKRRINALKQLQ	3319977 IN GenPept-1.pro			
80	DEDSADRPKGLIGYVLDTDFVSSLPPVKVKYRVLALKKLQ	5931610 IN GenPept-1.pro			
65	-----PKN-----DFISSLPPNSSLVLAALKKLQ	hNARC10C orf1-1.pro			
80	DEDSDDRPKGLIGYLLDTHSDFVSSLPPVKVKYRVLALKKLQ	P51860 IN SwissProt-1.pro			
38	-----HSDVLETLSPNVKRVESLREIQ	1161252 IN GenPept-1.pro			
	130	140	150	160	
75	VRGAHIEAKFFYEELVHDDLERRKYAALYQPLFFDKRREFITGDV	Q99733 IN SwissProt-1.pro			
75	VRGAHIEAKFFYEELVHDDLERRKYAALYQPLFFDKRREFITGDV	3319977 IN GenPept-1.pro			
120	TRGANLESAKFFLREREFHDLERRKFAEMYYQPLLEKKIQELTGEN	5931610 IN GenPept-1.pro			
89	KRGDKIEAKFFLREREFHDLERRKFAEMYYQPLLEKKIQELTGEN	hNARC10C orf1-1.pro			
120	TRGAHLESAKFFLREREFHDLERRKFAEMYYQPLLEKKIQELTGEN	P51860 IN SwissProt-1.pro			
61	GKHDELLEADFLKEREALAEAKYQKLYQPLLYTKRVEIVNGVT	1161252 IN GenPept-1.pro			

FIG. 1A

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ALIGNMENT REPORT OF UNTITLED, USING CLUSTAL METHOD WITH PAM250 RESIDUE WEIGHT TABLE.

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FIG. 1B

ALIGNMENT REPORT OF UNTITLED, USING CLUSTAL METHOD WITH PAM250 RESIDUE WEIGHT TABLE.

	330	340	350	360	
238	S F E G P E I V D C D G C T I D W K K G K N V T V K T I K K K Q K H K G R G T V				Q99733 IN SwissProt-1.pro
238	S F E G P E I V D C D G C T I D W K K G K N V T V K T I K K K Q K H K G R G T V				3319977 IN GenPept-1.pro
319	P Y R G T A I E Y S T G C E I D W N E G K N V T L K T I K K K Q K H R I W G T I				5931610 IN GenPept-1.pro
179	- -				hNARC10C orf1-1.pro
319	P Y R G T A I E Y A T G C D I D W N E G K N V T L R T I K K K Q R H R V W G T V				P51860 IN SwissProt-1.pro
191	- - D E P I L E K A I G T E I E W Y P G K C L T Q K V L K K K P K - K G S K N A				1161252 IN GenPept-1.pro
	370	380	390	400	
278	R T I T K Q V P N E S F F N F F N P L K A S G D G E S L D E D S E F T L A S - -				Q99733 IN SwissProt-1.pro
278	R T I T K Q V P N E S F F N F F N P L K A S G D G E S L D E D S E F T L A S - -				3319977 IN GenPept-1.pro
359	R T V T E D F P K D S F F N F F S P H G I T S N G R D G N D D - - - - -				5931610 IN GenPept-1.pro
179	- -				hNARC10C orf1-1.pro
359	R T V T E D F P K D S F F N F F S P H G I S L N G V E N D D - - - - -				P51860 IN SwissProt-1.pro
228	K P I T K T E S C E S F F N F F K P P E V P E D D A D I D E D L A E E L Q N Q M				1161252 IN GenPept-1.pro
	410	420	430	440	
316	- - D F E I G H F F R E R I V P R A V L Y F F T G E A I E D D D N - - F E E G E E				Q99733 IN SwissProt-1.pro
316	- - D F E I G H F F R E R I V P R A V L Y F F T G E A I E D D D N - - F E E G E E				3319977 IN GenPept-1.pro
390	- - F L L G H N L R T Y I I P R S V L F F S G D A L E S Q Q E G V V R E V N D				5931610 IN GenPept-1.pro
179	- -				hNARC10C orf1-1.pro
390	- - F L L G H N L R T Y I I P R S V L F F S G D A L E S Q Q E G V V R E V N D				P51860 IN SwissProt-1.pro
268	E Q D Y D L G S T L R D K I I P H A V S W F T G E A A Q G D E F E D L E D D E D				1161252 IN GenPept-1.pro
	450	460	470	480	
352	G E E E E L E G D E - - E G E D E D D A - - - E I N P K V				Q99733 IN SwissProt-1.pro
352	G E E E E L E G D E - - E G E D E D D A - - - D V N P K V				3319977 IN GenPept-1.pro
427	A I Y D K I I Y D N W M A A I E E V K A C C K N L E A L V E D I D R				5931610 IN GenPept-1.pro
179	- -				hNARC10C orf1-1.pro
427	E I Y D K I I Y D D W M A A I E E V K A C C K N L E A L V E D I D R				P51860 IN SwissProt-1.pro
308	E E E D E D E D E D E D E D E D E D E D E D T K T K K K S G K A Q A G D G				1161252 IN GenPept-1.pro

FIG. 1C

10047855 060600

Title: NARC 10 and NARC 16, Programmed Cell  
 Death-Associated Molecules and Uses Thereof  
 Inventor(s): Chiang  
 Application No: 10/047,855  
 Atty Dkt No: 35800/242056(5800-190)

ALIGNMENT REPORT OF UNTITLED, USING CLUSTAL METHOD WITH PAM250 RESIDUE WEIGHT TABLE.

375		Q99733 IN SwissProt-1.pro
375		3319977 IN GenPept-1.pro
460		5931610 IN GenPept-1.pro
182		hNARC10C orf1-1.pro
460		P51860 IN SwissProt-1.pro
348	D G E R P P E C K Q Q	1161252 IN GenPept-1.pro

FIG. 1D

10047855.060602

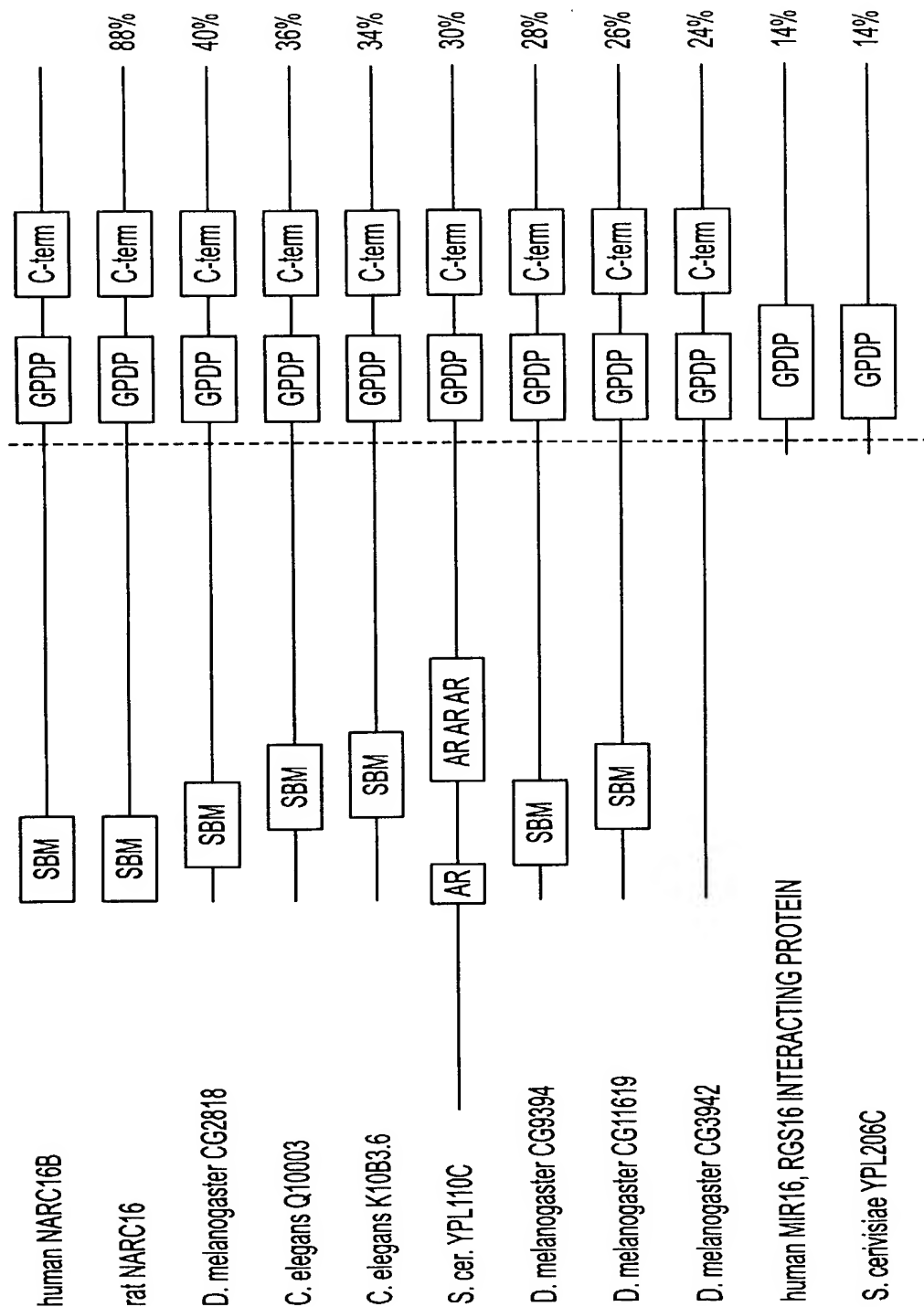


FIG. 2

ALIGNMENT REPORT OF truncatedNARC16GPDpClustal.MEG, USING CLUSTAL METHOD WITH PAM250 RESIDUE WEIGHT TABLE.

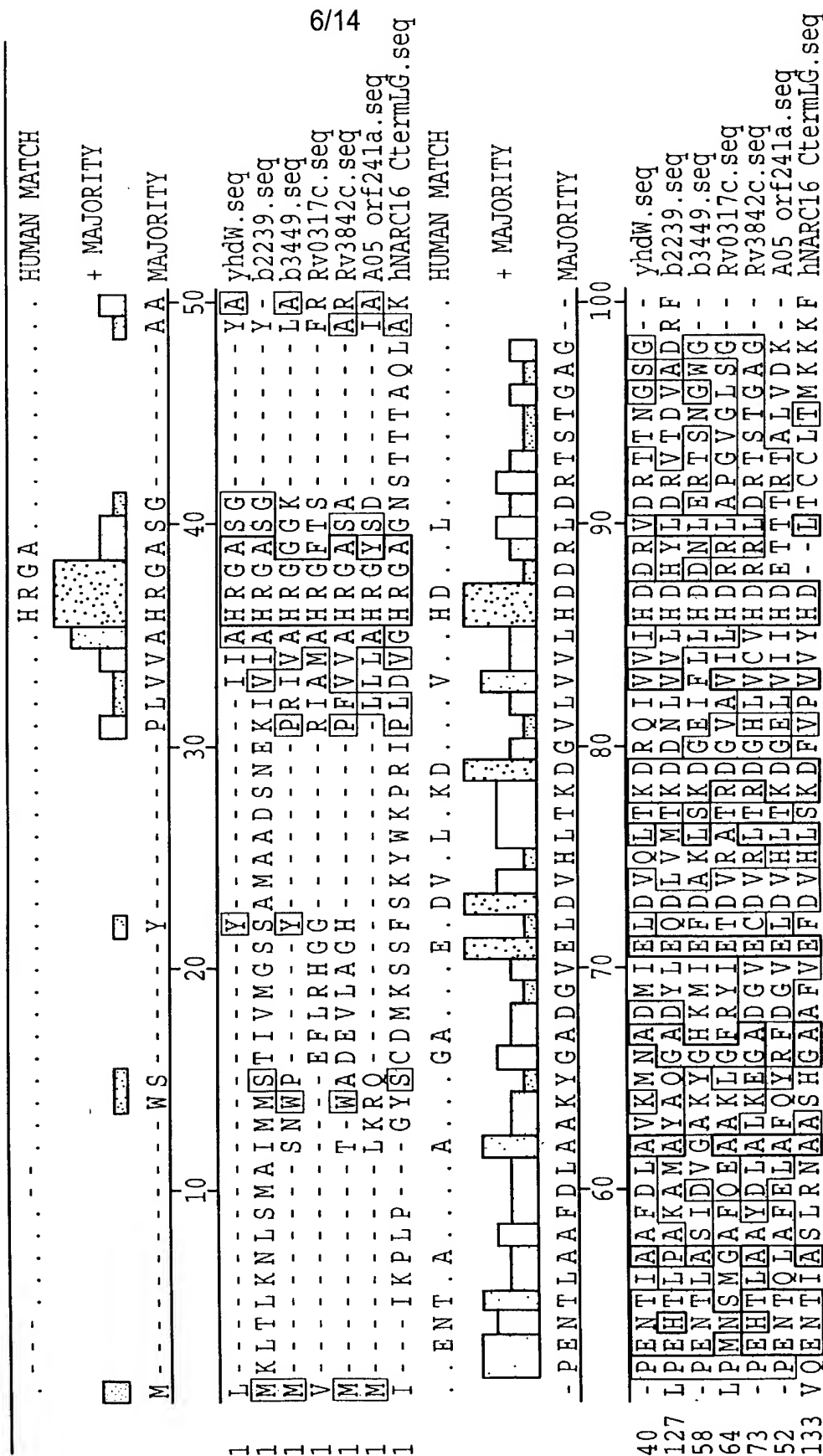


FIG. 3A

ALIGNMENT REPORT OF truncatedNARC16GPDPolustal.MEG, USING CLUSTAL METHOD WITH PAM250 RESIDUE WEIGHT TABLE.

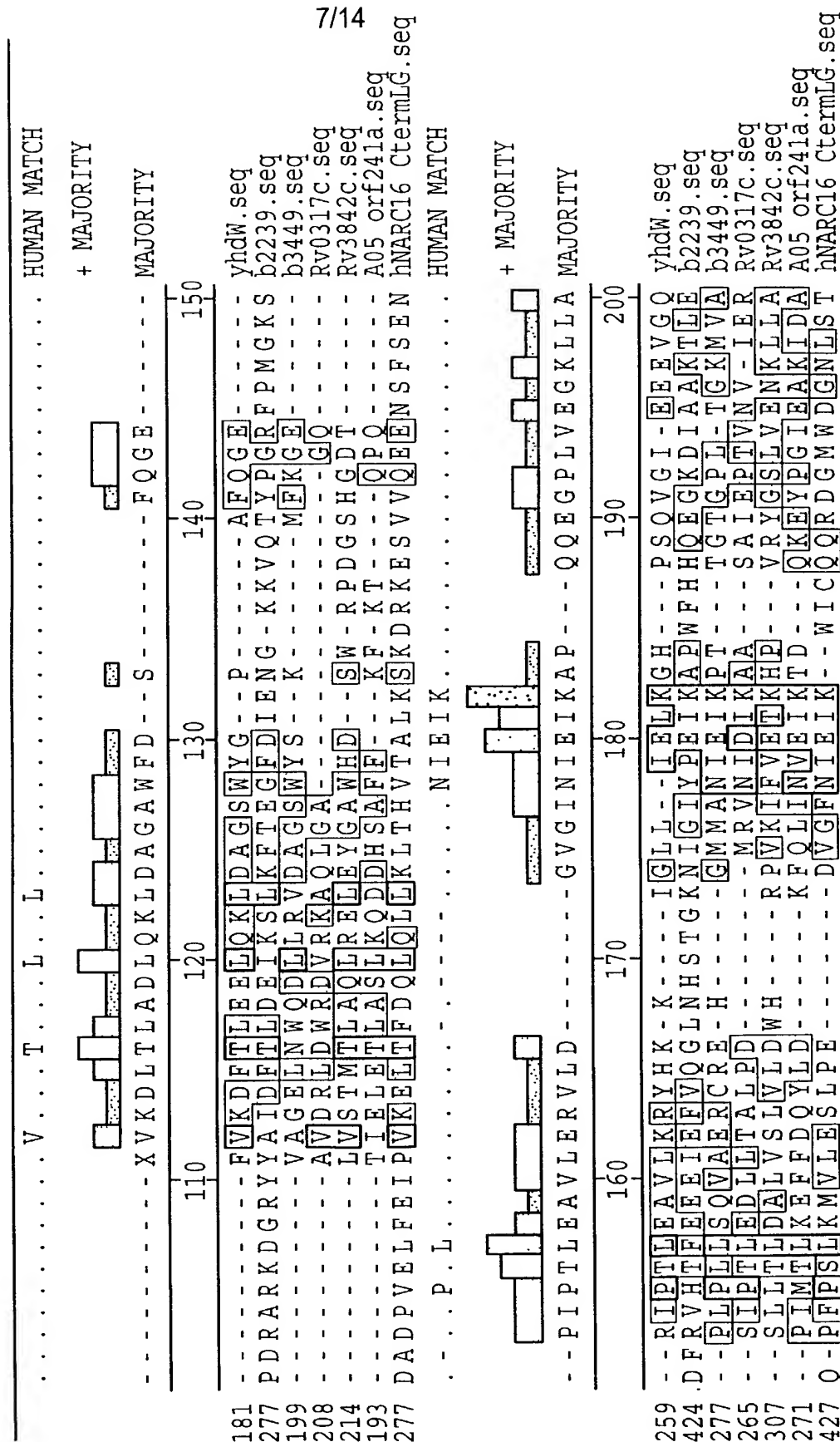


FIG. 3B

ALIGNMENT REPORT OF truncatedNARC16GPPDclusta.MEG, USING CLUSTAL METHOD WITH PAM250 RESIDUE WEIGHT TABLE.

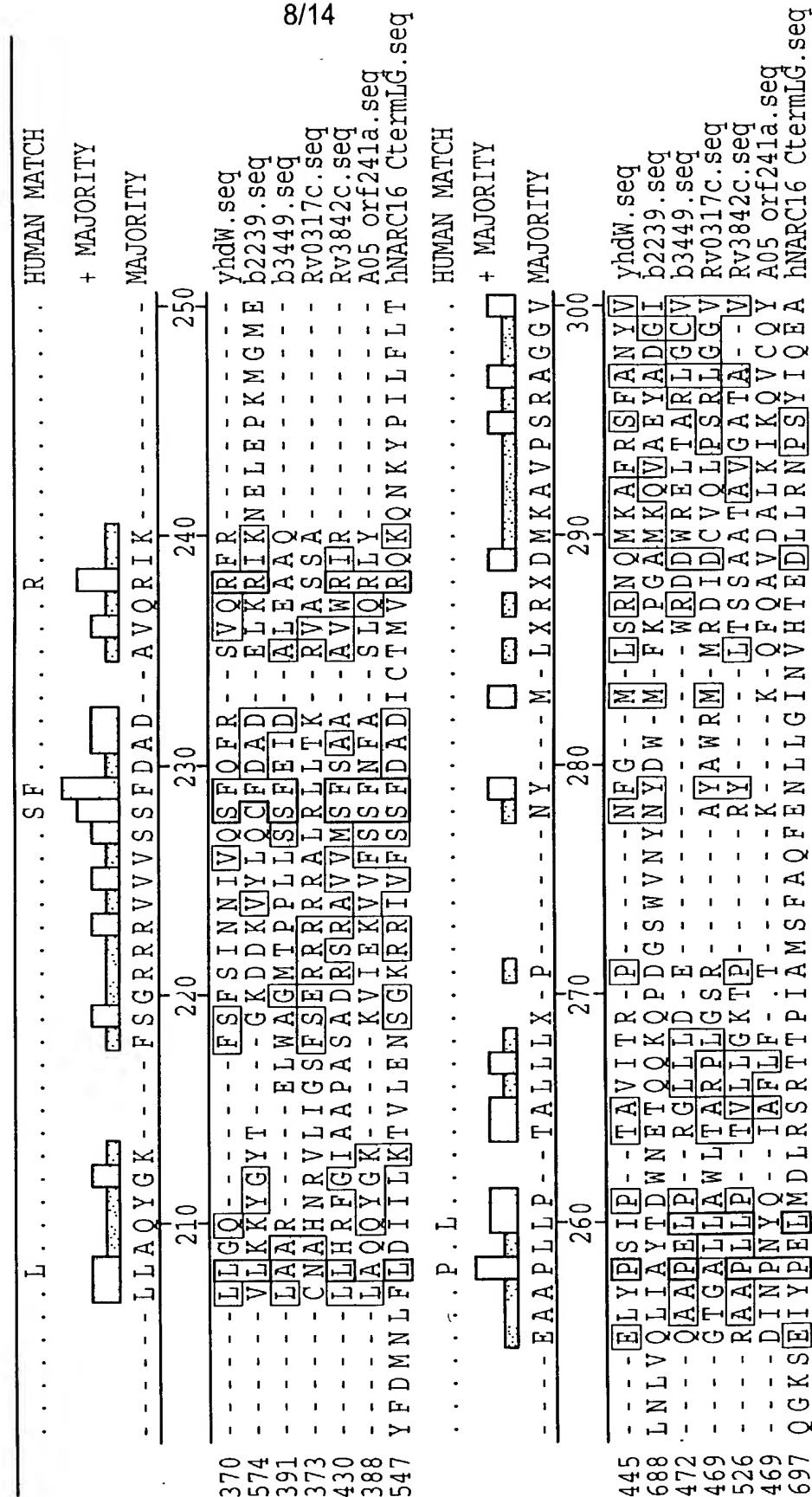


FIG. 3C



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FIG. 3D

Title: NARC 10 and NARC 16, Programmed Cell  
 Death-Associated Molecules and Uses Thereof  
 Inventor(s): Chiang  
 Application No: 10/047,855  
 Atty Dkt No: 35800/242056(5800-190)

# ALIGNMENT REPORT OF truncatedNARC16GPDpClustal.MEG, USING CLUSTAL METHOD WITH PAM250 RESIDUE WEIGHT TABLE.

	HUMAN MATCH
730	+ MAJORITY
1075	MAJORITY
742	yhdW.seq
769	b2239.seq
823	b3449.seq
724	Rv0317c.seq
1138	Rv3842c.seq
	A05 orf241a.seq
	hNARC16 CtermLG.seq

10/14

10047855.060602

FIG. 3E

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INPUT FILE flhbNARC10C; OUTPUT FILE flhbNARC10C.pat  
SEQUENCE LENGTH 2034

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      M A D S E N Q G P A E P S Q A A 16
GGCTTCTCTCTAAC ATG GCC GAC TCG GAA AAC CAG GGG CCT GCG GAG CCT AGC CAG GCG GCG 142
A A A E A A A E E V M A E G G A O G G D 36
GCA GCG GCG GAG GCA GCG GCA GAG GAG GTA ATG GCG GAA GGC GGT GCG CAG GGT GGA GAC 202
C D S A A G D P D S A A G Q M A E E P Q 56
TGT GAC AGC GCG GCT GGT GAC CCT GAC AGC GCG GCT GGT CAG ATG GCT GAG GAG CCC CAG 262
T P A E N A P K P K N D F I E S L P N S 76
ACC CCT GCA GAG AAT GCC CCA AAG CCG AAA AAT GAC TTT ATC GAG AGC CTG CCT AAT TCG 322
V K C R V L A L K K L Q K R C D K I E A 96
GTG AAA TGC CGA GTC CTG GCC CTC AAA AAG CTG CAG AAG CGA TGC GAT AAG ATA GAA GCC 382
K F D K E F Q A L E K K Y N D I Y K P L 116
AAA TTT GAT AAG GAA TTT CAG GCT CTG GAA AAA AAG TAT AAT GAC ATC TAT AAG CCC CTA 442
L A K I Q E L T G E M E G C A W T L E G 136
CTC GCC AAG ATC CAA GAG CTC ACC GGC GAG ATG GAG GGG TGT GCA TGG ACC TTG GAG GGG 502
E E E E E E E Y E D D E E E G E D E E E 156
GAG GAG GAG GAG GAA GAG GAG TAC GAG GAT GAC GAG GAG GAG GGG GAA GAC GAG GAG GAG 562
E E A A A E A A A G A K H D D A H A E M 176
GAG GAG GCT GCG GCA GAG GCT GCC GCG GGG GCC AAA CAT GAC GAT GCC CAC GCC GAG ATG 622
P D D A K K * 183
CCT GAT GAC GCC AAG AAG TAA 643
GGGGGGCAGAGATGGATGAAGAGAAAGCCACGAAGAAAAAGCCTGGTTTTGTGTTTCCCAAGATATCGATGGACTTA 722
AAAAGGCTCAGGTTTTTGACCAAAATACAATGTGAATTTATTCTGACATTCCTAAAATAGATTAAATTAAGCAATTAG 801
ATCCTGGCCAGCTCGATTCAAATTTGACTTTTCATTTTGAACATAATAAATATATCAAAGGTGTTAAAGAAAACTGAAT 880
TAAACCCAAAATTATGTTTTCATGGTCTCTTCTCTGAGGATTGAGGTTTACAAAGGGTGTTAGCAGATGCGAAGTAAAG 959
AACGTCACTTTGAAACCCATTCATCACACAGCATACGCTACACATGGAACCCCAAGCCATGACTGAACACGTTCTCAG 1038
TGCTTAATTCCTAAATTTCTTTACTCATGACATTTTCGCACTGCAGAGAAGGCAGAACCCCAAGAAAAACGTCACTTTGA 1117
GACTTTGCTTTTGTAAACGAGACATCAGCTTTTCACTTCACAGGAGATTGATGGCATTGAGGAAGATTGCAATGGAGAT 1196
CATGACACTACTGTTAATAAGGCCAGGAAAACTGCCATTTCAAGTTCTGAAAAATGTTTGTAGTATTTGAATTTAGAGA 1275
AACACATGGTTCCAAGAAGGAGGGTGTAACCTGTAAATACTGTCAACATATGTATTATTAGTTACAATCTCATG 1354
TTTGTGTTTTCTTAGTACTGTCTATTTACAAACACGTAAAAATACCCCAAATATGTTTAAGTATTAAATCACTTTACC 1433
TAGCGTTTTAGAAAATATTAATTTACTTGAAGAGATGTAGAATGTAGCAAATATGTAAAGCATGTGTATCCAGCGTTAT 1512
GTACTTTGCGCCTTGTGACGTCTTTCTGTCATGTAGCTTTTAGGGTGTAGCTGTGAAAATCATCAGAACTCTTCACTGA 1591
AGCTAATGTTTGAAAAAATATATACTTGAAGAACCAATCCAAGTGTGTGCCCCCTACCCCAAGCTCAGAAGTAGAAAGG 1670
GTTTAAGTTTGCTTGTATTAGCTGTGCCTTCATTATTTTGTATGTAATGTGACATATTAATTATAAAATGGTGCATA 1749
ATCAAATTTTACTGCTTGAGGACAGATGCATACAGTAAGGATTTTTAGGAAGAATATATTTAATGTAAAGACTCTTAGC 1828
TTCTGTGTGGGTTTTGAATTATGTGTGAGCCAGTGATCTATAAAGAAACATAAGCTTAAAGTTGTTTATCACTGTGGTG 1907
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SEQUENCE LENGTH 3206

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      M T P 3
GGCGGCGACGCGGACCTGCGGACTAGCGAACCCGGAGCAGACATCATAAAATAAATCCATCAGA ATG ACA CCT 153
S O V A F E I R G T L L P G E V F A I C 23
TCT CAG GTT GCC TTT GAA ATA AGA GGA ACT CTT TTA CCA GGA GAA GTT TTT GCG ATA TGT 213
```

FIG. 4A

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G	S	C	D	A	L	G	N	W	N	P	Q	N	A	V	A	L	L	P	E	43
GGA	AGC	TGT	GAT	GCT	TTG	GGA	AAC	TGG	AAT	CCT	CAA	AAT	GCT	GTG	GCT	CTT	CTT	CCA	GAG	273
N	D	T	G	E	S	M	L	W	K	A	T	I	V	L	S	R	G	V	S	63
AAT	GAC	ACA	GGT	GAA	AGC	ATG	CTA	TGG	AAA	GCA	ACC	ATT	GTA	CTC	AGT	AGA	GGA	GTA	TCA	333
V	Q	Y	R	Y	F	K	G	Y	F	L	E	P	K	T	I	G	G	P	C	83
GTT	CAG	TAT	CGC	TAC	TTC	AAA	GGG	TAC	TTT	TTA	GAA	CCA	AAG	ACT	ATC	GGT	GGT	CCA	TGT	393
Q	V	I	V	H	K	W	E	T	H	L	Q	P	R	S	I	T	P	L	E	103
CAA	GTG	ATA	GTT	CAC	AAG	TGG	GAG	ACT	CAT	CTA	CAA	CCA	CGA	TCA	ATA	ACC	CCT	TTA	GAA	453
S	E	I	I	I	D	D	G	Q	F	G	I	H	N	G	V	E	T	L	D	123
AGC	GAA	ATT	ATT	ATT	GAC	GAT	GGA	CAA	TTT	GGA	ATC	CAC	AAT	GGT	GTT	GAA	ACT	CTG	GAT	513
S	G	W	L	T	C	Q	T	E	I	R	L	R	L	H	Y	S	E	K	P	143
TCT	GGA	TGG	CTG	ACA	TGT	CAG	ACT	GAA	ATA	AGA	TTA	CGT	TTG	CAT	TAT	TCT	GAA	AAA	CCT	573
P	V	S	I	T	K	K	K	L	K	K	S	R	F	R	V	K	L	T	L	163
CCT	GTG	TCA	ATA	ACC	AAG	AAA	AAA	TTA	AAA	AAA	TCT	AGA	TTT	AGG	GTG	AAG	CTG	ACA	CTA	633
E	G	L	E	E	D	D	D	D	R	V	S	P	T	V	L	H	K	M	S	183
GAA	GAC	CTG	GAG	GAA	GAT	GAC	GAT	GAG	AGG	GTA	TCT	CCC	ACT	GTA	CTC	CAC	AAA	ATG	TCC	693
N	S	L	E	I	S	L	I	S	D	N	E	F	K	C	R	H	S	Q	P	203
AAT	AGC	TTG	GAG	ATA	TCC	TTA	ATA	AGC	GAC	AAT	GAG	TTC	AAG	TGC	AGG	CAT	TCA	CAG	CCG	753
E	C	G	Y	G	L	Q	P	D	R	W	T	E	Y	S	I	Q	T	M	E	223
GAG	TGT	GGT	TAT	GGC	TTG	CAG	CCT	GAT	CGT	TGG	ACA	GAG	TAC	AGC	ATA	CAG	ACG	ATG	GAA	813
P	D	N	L	E	L	I	F	D	F	F	E	E	D	L	S	E	H	V	V	243
CCA	GAT	AAC	CTG	GAA	CTA	ATC	TTT	GAT	TTT	TTC	GAA	GAA	GAT	CTC	AGT	GAG	CAC	GTA	GTT	873
Q	G	D	A	L	P	G	H	V	G	T	A	C	L	L	S	S	T	I	A	263
CAG	GGT	GAT	GCC	CTT	CCT	GGA	CAT	GTG	GGT	ACA	GCT	TGT	CTC	TTA	TCA	TCC	ACC	ATT	GCT	933
E	S	G	K	S	A	G	I	L	T	L	P	I	M	S	R	N	S	R	K	283
GAG	AGT	GGA	AAG	AGT	GCT	GGA	ATT	CTT	ACT	CTT	CCC	ATC	ATG	AGC	AGA	AAT	TCC	CGG	AAA	993
T	I	G	K	V	R	V	D	Y	I	I	I	K	P	L	P	G	Y	S	C	303
ACA	ATA	GGC	AAA	GTG	AGA	GTT	GAC	TAT	ATA	ATT	ATT	AAG	CCA	TTA	CCA	GGA	TAC	AGT	TGT	1053
D	M	K	S	S	F	S	K	Y	W	K	P	R	I	P	L	D	V	G	H	323
GAC	ATG	AAA	TCT	TCA	TTT	TCC	AAG	TAT	TGG	AAG	CCA	AGA	ATA	CCA	TTG	GAT	GTT	GGC	CAT	1113
R	G	A	G	N	S	T	T	T	A	Q	L	A	K	V	Q	E	N	T	I	343
CGA	GGT	GCA	GGA	AAC	TCT	ACA	ACA	ACT	GCC	CAG	CTG	GCT	AAA	GTT	CAA	GAA	AAT	ACT	ATT	1173
A	S	L	R	N	A	A	S	H	G	A	A	F	V	E	F	D	V	H	L	363
GCT	TCT	TTA	AGA	AAT	GCT	GCT	AGT	CAT	GGT	GCA	GCC	TTT	GTA	GAA	TTT	GAC	GTA	CAC	CTT	1233
S	K	D	F	V	P	V	V	Y	H	D	L	T	C	C	L	T	M	K	K	383
TCA	AAG	GAC	TTT	GTG	CCC	GTG	GTA	TAT	CAT	GAT	CTT	ACC	TGT	TGT	TTG	ACT	ATG	AAA	AAG	1293
K	F	D	A	D	P	V	E	L	F	E	I	P	V	K	E	L	T	F	D	403
AAA	TTT	GAT	GCT	GAT	CCA	GTT	GAA	TTA	TTT	GAA	ATT	CCA	GTA	AAA	GAA	TTA	ACA	TTT	GAC	1353
Q	L	Q	L	L	K	L	T	H	V	T	A	L	K	S	K	D	R	K	E	423
CAA	CTC	CAG	TTG	TTA	AAG	CTC	ACT	CAT	GTG	ACT	GCA	CTG	AAA	TCT	AAG	GAT	CGG	AAA	GAA	1413
S	V	V	Q	E	E	N	S	F	S	E	N	Q	P	F	P	S	L	K	M	443
TCT	GTG	GTT	CAG	GAG	GAA	AAT	TCC	TTT	TCA	GAA	AAT	CAG	CCA	TTT	CCT	TCT	CTT	AAG	ATG	1473
V	L	E	S	L	P	E	D	V	G	F	N	I	E	I	K	W	I	C	Q	463
GTT	TTA	GAG	TCT	TTG	CCA	GAA	GAT	GTA	GGG	TTT	AAC	ATT	GAA	ATA	AAA	TGG	ATC	TGC	CAG	1533
Q	R	D	G	M	W	D	G	N	L	S	T	Y	F	D	M	N	L	F	L	483
CAA	AGG	GAT	GGA	ATG	TGG	GAT	GGT	AAC	TTA	TCA	ACA	TAT	TTT	GAC	ATG	AAT	CTG	TTT	TTG	1593
D	I	I	L	K	T	V	L	E	N	S	G	K	R	R	I	V	F	S	S	503
GAT	ATA	ATT	TTA	AAA	ACT	GTT	TTA	GAA	AAT	TCT	GGG	AAG	AGG	AGA	ATA	GTG	TTT	TCT	TCA	1653
F	D	A	D	I	C	T	M	V	R	Q	K	Q	N	K	Y	P	I	L	F	523
TTT	GAT	GCA	GAT	ATT	TGC	ACA	ATG	GTT	CGG	CAA	AAG	CAG	AAC	AAA	TAT	CCG	ATA	CTA	TTT	1713
L	T	Q	G	K	S	E	I	Y	P	E	L	M	D	L	R	S	R	T	T	543
TTA	ACT	CAA	GGA	AAA	TCT	GAG	ATT	TAT	CCT	GAA	CTC	ATG	GAC	CTC	AGA	TCT	CGG	ACA	ACC	1773
P	I	A	M	S	F	A	Q	F	E	N	L	L	G	I	N	V	H	T	E	563
CCC	ATT	GCA	ATG	AGC	TTT	GCA	CAG	TTT	GAA	AAT	CTA	CTG	GGG	ATA	AAT	GTA	CAT	ACT	GAA	1833

FIG. 4B

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D L L R N P S Y I Q E A K A K G L V I F 583
GAC TTG CTC AGA AAC CCA TCC TAT ATT CAA GAG GCA AAA GCT AAG GGA CTA GTC ATA TTC 1893
C W G D D T N D P E N R R K L K E L G V 603
TGC TGG GGT GAT GAT ACC AAT GAT CCT GAA AAC AGA AGG AAA TTG AAG GAA CTT GGA GTT 1953
N G L I Y D R I Y D W M P E Q P N I F Q 623
AAT GGT CTA ATT TAT GAT AGG ATA TAT GAT TGG ATG CCT GAA CAA CCA AAT ATA TTC CAA 2013
V E Q L E R L K Q E L P E L K S C L C P 643
GTG GAG CAA TTG GAA CGC CTG AAG CAG GAA TTG CCA GAG CTT AAG AGC TGT TTG TGT CCC 2073
T V S R F V P S S L C G E S D I H V D A 663
ACT GTT AGC CGC TTT GTT CCC TCA TCT TTG TGT GGG GAG TCT GAT ATC CAT GTG GAT GCC 2133
N G I D N V E N A * 673
AAC GGC ATT GAT AAC GTG GAG AAT GCT TAG 2163
TTTTTATGACAGAGGTCAATTTTGGGGCGTGCACCGCTGTTCTGGGTATTCATTTTTCATCACTGAGCATTGTTGAT 2242
CTATGCCCTTTTGGGCTTCTCAGTTCAATGAAGCAATAATGAAGTATTTAACTCTTTCACCTACAGTTCCTGCAAGTATGC 2321
TATTTAAATTACTTGCCAGGTATAATTGCCAGTCAGTCTCTTTATAGTGAGAAAATTTATTGGTTAGTAATATAAATA 2400
TTTTAACTAAATATATAAATCTATAATGTTAAACATATGTTCAATTAAGCATAGCACTTTGAAATTAATATATAAA 2479
TAGCTCATATTTTACACTTACAGCTTTTCATTTGATCAGGTCTGAAATCTTTAGCACTTAAGGAAAATGACTATGCATAA 2558
TTATACCTGACCATGAAAAAATAAGTACCTCAAATGCATGCATTTGCACTGGTGATTCCAATGCACAAATCTTTGTG 2637
CCATCTTGATATAGGTATTTTTTACATGGGTGACATGCACACAACACCATTTTCATTCAGTATGAACCTTGAGGCTG 2716
CTGCCATTTTTCACCTTAACCAACCCAGCCTGAAGGTGAACCTCGAACTTGTTTCATAAATCTTTCAAAAGTTGTTTT 2795
ACATCAATGTTAAATTTCAAAATGCTGCAGGGTAATTTAATGTATAAAATATTAGTAAGAAAAAGTATGTATGCATA 2874
CTTAGTAGAATAGATCACAACATACAAATTCATTCAGTGCATGCTTTAGGTGTTAAGCATGAGATTGTACATGTTTAC 2953
TGTTAGGTCCTTGATCTGTGGTGCTAGGTGAGTATGAGAAGATGTCAAGGACTGGACGTATTTTGTTCCTAAAAAA 3032
AAAGGCTGTTTGTAGGCGTTTAAATATGCTTATTTTGTGTGTCTCTCACTACCTATTACACACTGTTGCTTTGTGGGT 3111
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AAAAAGGGCGGCCGC 3206
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FIG. 4C

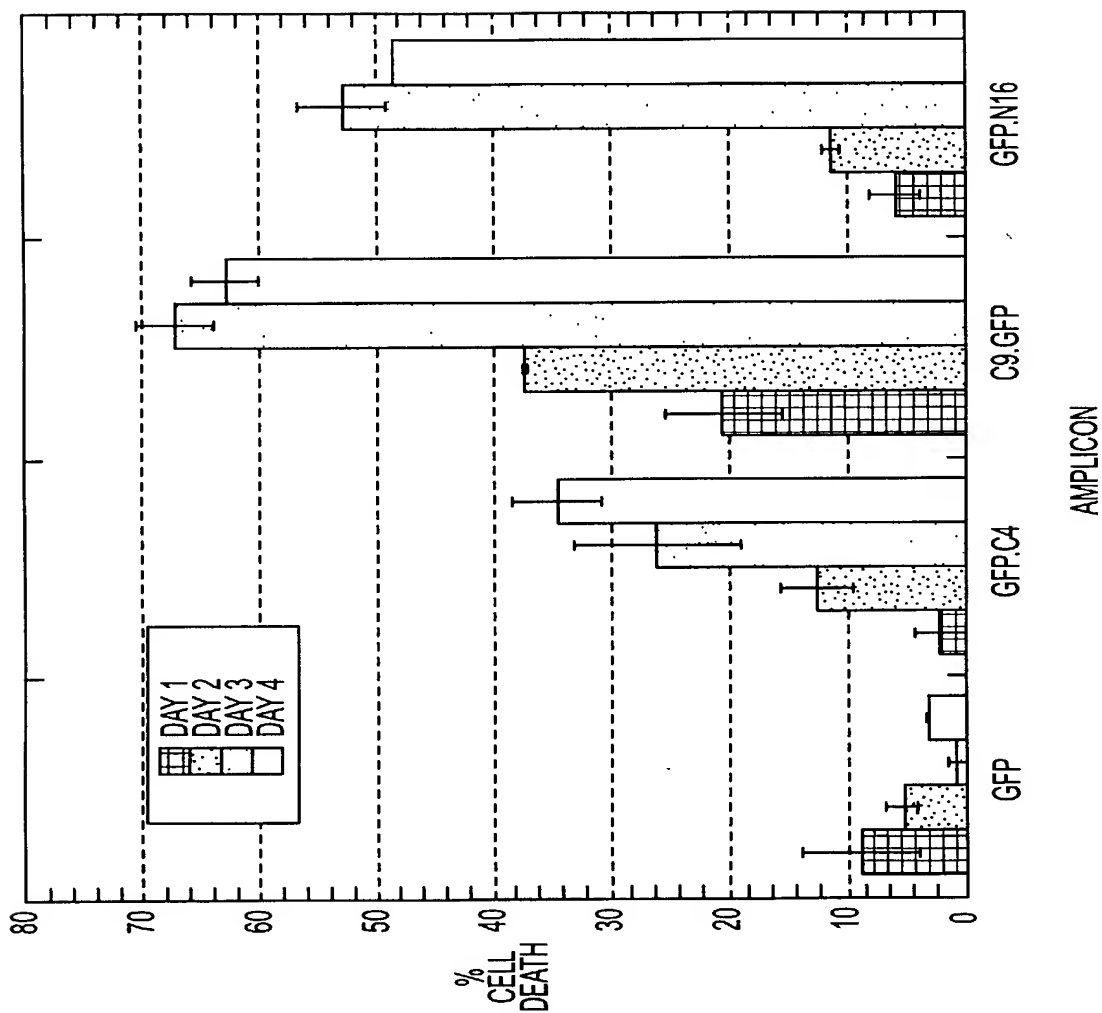


FIG. 5